

SEQUENCE LISTING

<110> Poch, Jean-Marc
 Bartel, Paul L.
 Reichman, Karen

<120> Protein-Protein Interactions in Neurodegenerative
 Diseases

<130> Protein Interactions in ND

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<150> US 60/240,790

<151> 2000-10-17

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:tail for
 forward primer for yeast two-hybrid system

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<223> Description of Artificial Sequence:tail for
 reverse primer for yeast two-hybrid system

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<213> Homo sapiens

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<221> CDS

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taattaaaaa atttttcagg gacgtagcaa tccagagaca ttccattatt gttccattga 180

cctttccctc atcaactgagt cctttggagg tgagtt atg tca aca gct gcc tta 234

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Ile	Thr	Leu	Val	Arg	Ser	Gly	Gly	Asn	Gln	Val	Arg	Arg	Arg	Val	Leu	
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cta	agc	tcc	cgc	ctg	ctg	cag	gac	gac	agg	egg	gtg	aca	ccc	acg	tgc	330
Leu	Ser	Ser	Arg	Leu	Leu	Gln	Asp	Asp	Arg	Arg	Val	Thr	Pro	Thr	Cys	
		25					30					35				
cac	agc	tcc	act	tca	gag	cct	agg	tgt	tct	egg	ttt	gac	cca	gat	ggt	378
His	Ser	Ser	Thr	Ser	Glu	Pro	Arg	Cys	Ser	Arg	Phe	Asp	Pro	Asp	Gly	
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agt	ggg	agt	cca	gct	acc	tgg	gac	aat	ttt	ggg	atc	tgg	gat	aac	cgc	426
Ser	Gly	Ser	Pro	Ala	Thr	Trp	Asp	Asn	Phe	Gly	Ile	Trp	Asp	Asn	Arg	
	55			60						65					70	
att	gat	gag	cca	att	ctg	ctg	cca	ccc	agc	att	aag	tat	ggc	aag	cca	474
Ile	Asp	Glu	Pro	Ile	Leu	Leu	Pro	Pro	Ser	Ile	Lys	Tyr	Gly	Lys	Pro	
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att	ccc	aaa	atc	agc	ttg	gaa	aat	gtg	ggg	tgc	gcc	tca	cag	att	ggc	522
Ile	Pro	Lys	Ile	Ser	Leu	Glu	Asn	Val	Gly	Cys	Ala	Ser	Gln	Ile	Gly	
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Lys	Arg	Lys	Glu	Asn	Glu	Asp	Arg	Phe	Asp	Phe	Ala	Gln	Leu	Thr	Asp	
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Glu	Val	Leu	Tyr	Phe	Ala	Val	Tyr	Asp	Gly	His	Gly	Gly	Pro	Ala	Ala	
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gct	gat	ttc	tgt	cat	acc	cac	atg	gag	aaa	tgt	att	atg	gat	ttg	cct	666
Ala	Asp	Phe	Cys	His	Thr	His	Met	Glu	Lys	Cys	Ile	Met	Asp	Leu	Leu	
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cct	aag	gag	aag	aac	ttg	gaa	act	ctg	ttg	acc	ttg	gct	ttt	cta	gaa	714
Pro	Lys	Glu	Lys	Asn	Leu	Glu	Thr	Leu	Leu	Thr	Leu	Ala	Phe	Leu	Glu	
				155				160						165		
ata	gat	aaa	gcc	ttt	tgg	agt	cat	gcc	cgc	ctg	tct	gct	gat	gca	act	762
Ile	Asp	Lys	Ala	Phe	Ser	Ser	His	Ala	Arg	Leu	Ser	Ala	Asp	Ala	Thr	
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cct	ctg	acc	tct	ggg	act	act	gca	aca	gta	gcc	cta	ttg	cga	gat	ggt	810
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Ile	Glu	Leu	Val	Val	Ala	Ser	Val	Gly	Asp	Ser	Arg	Ala	Ile	Leu	Cys	
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aga	aaa	gga	aaa	ccc	atg	aag	ctg	acc	att	gac	cat	act	cca	gaa	aga	906
Arg	Lys	Gly	Lys	Pro	Met	Lys	Leu	Thr	Ile	Asp	His	Thr	Pro	Glu	Arg	
	215				220					225				230		
aaa	gat	gaa	aaa	gaa	agg	atc	aag	aaa	tgt	ggt	ggt	ttt	gta	gct	tgg	954
Lys	Asp	Glu	Lys	Glu	Arg	Ile	Lys	Lys	Cys	Gly	Gly	Phe	Val	Ala	Trp	
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 tgttttgtaa ttaccaaaag tactacctga gtgtataatg actccgcag tgagttaatg 2592
 taattgctgc ttgaccatt gttttaaatc tgtgtactag agtaactgtg agcagaatga 2652
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 <212> PRT
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 35 40 45
 Arg Phe Asp Pro Asp Gly Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe
 50 55 60
 Gly Ile Trp Asp Asn Arg Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser
 65 70 75 80
 Ile Lys Tyr Gly Lys Pro Ile Pro Lys Ile Ser Leu Glu Asn Val Gly
 85 90 95
 Cys Ala Ser Gln Ile Gly Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp
 100 105 110
 Phe Ala Gln Leu Thr Asp Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly
 115 120 125
 His Gly Gly Pro Ala Ala Ala Asp Phe Cys His Thr His Met Glu Lys
 130 135 140
 Cys Ile Met Asp Leu Leu Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu
 145 150 155 160
 Thr Leu Ala Phe Leu Glu Ile Asp Lys Ala Phe Ser Ser His Ala Arg
 165 170 175
 Leu Ser Ala Asp Ala Thr Leu Leu Thr Ser Gly Thr Thr Ala Thr Val
 180 185 190
 Ala Leu Leu Arg Asp Gly Ile Glu Leu Val Val Ala Ser Val Gly Asp
 195 200 205
 Ser Arg Ala Ile Leu Cys Arg Lys Gly Lys Pro Met Lys Leu Thr Ile
 210 215 220

Asp His Thr Pro Glu Arg Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys
 225 230 235 240
 Gly Gly Phe Val Ala Trp Asn Ser Leu Gly Gln Pro His Val Asn Gly
 245 250 255
 Arg Leu Ala Met Thr Arg Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser
 260 265 270
 Gly Val Ile Ala Glu Pro Glu Thr Lys Arg Ile Lys Leu His His Ala
 275 280 285
 Asp Asp Ser Phe Leu Val Leu Thr Thr Asp Gly Ile Asn Phe Met Val
 290 295 300
 Asn Ser Gln Glu Ile Cys Asp Phe Val Asn Gln Cys His Asp Pro Asn
 305 310 315 320
 Glu Ala Ala His Ala Val Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu
 325 330 335
 Asp Asn Ser Thr Ala Val Val Val Pro Phe Gly Ala Trp Gly Lys Tyr
 340 345 350
 Lys Asn Ser Glu Ile Asn Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser
 355 360 365
 Gly Arg Trp Ala
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